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GenCore version 4.5
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   Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 30, 2002, 15:43:51 ; Search time 32.5 Seconds (without alignments) 1240.609 Million cell updates/sec

Title: Perfect score: US-09-769-787-162 1843

Sequence: 1 MSEIKIINAKKIYHDVPVIE.....LNIFSADGSQNLIKGVNHGT

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :	A_Geneseq_032802:*
	1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
	2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
	3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
	4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
	5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
	6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
	7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
	8: /SIDS1/gcgdata/hold-geneseg/genesegp-emb]/AA1987.DAT:*

9: 10: 11: 12: 13: 14: 15: 16: 16: 17: 19: 19: 20:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match Length DB	ength	DB	ID	Description
ם	1843	100.0	364	21	AAY81674	Streptococcus pneu
2	651.5	35.3	381	22	AAU35636	Haemophilus influe
ω	651	35.3	373	22	AAB96796	Putative P. abyssi
4	645.5	35.0	371	22	AAB96092	Putative P. abyssi
₅	638.5	34.6	352	22	AAU34460	E. coli cellular p
6	627.5	34.0	328	22	AAB88524	Haemophilus influe
7	625.5	33.9	329	22	AAB96235	Putative P. abyssi
80	623.5	33.8	364	22	AAG82000	S. epidermidis ope
9	620.5	33.7	369	22	AAB86541	E. rhapontici Palk
10	617.5	33.5	337	21	AAY81650	Streptococcus pneu
11	616	33.4	467	22	AAU59977	Propionibacterium

ALIGNMENTS

AAY81674 RESULT . .

AAY81674 standard; Protein; 364 A

AAY81674;

24-MAY-2000 (first entry)

Streptococcus pneumoniae protein sequence ID211 - 4127.2.

Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;

pneumococcal disease

Streptococcus pneumoniae.

WO200006737-A2.

FINANCE SERVICE SERVIC

Date no good for out

10-FEB-2000.

27-JUL-1999; 99WO-GB02451

27-JUL-1998; 19-MAR-1999; 98GB-0016337. 99US-0125164.

(MICR-) MICROBIAL TECHNICS LTD

Gilbert CFG, Hansbro PM;

WPI; 2000-195300/17.

New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein -

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RESULT
AAU35636
ID AAU3
XX AAU3
XX AAU3
XX AAU3
XX AAU4
DT 14-F
XX Anti
XX Anti
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XX Anti
XX Haen
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XX WO2(
PN WO2(
PD 27-9
XX 27-9
PF 21-1
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Best Local
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   21-MAR-2001; 2001WO-US09180
                                                             WO200170955-A2
                                                                                                                     Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                                                                  Haemophilus
                                                                                        Haemophilus influenzae
                                                                                                                                                                                               14-FEB-2002
                                                                                                                                                                                                                                                        AAU35636 standard; Protein;
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Pred. No. 2.3e-167;
; Mismatches 0;
                                                                                                                                                                proliferation protein #277.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an cessential prokaryotic cellular proliferation protein.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
Sequence
                                                                                                                                                                                                                                                                                                                                                                   Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                    antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto
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                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides for the identification and development
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DB; AAS53495.
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                                                                                                                                                                                                                                                                                                                                                                 Seq ID No 11229; 511pp; English.
381
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                  comprise sequences of antisense nucleic
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Xu HH;
AA;
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Query Match
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Matches 139
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                                                                                         GITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNIIPAN
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                                                                                                                     skaiighiidrtykgmtlestvefdhngmrvlvse--ffned
                    SGDIEGTIRDSVYLGLNTDYFIETGF-ASKIQVSEESTFEED
                                        vierkseqvvlanvegricdiytd----
                                                                             gitfifvthdqeeaitmsdrivllrkgkiaqdgspreiyedpanlfvarfigeinvfeat
                                                                                                                                  al Similarity
139; Conserv
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                                                                                                                                                                                                                                                       35.3%;
                                                          -VFSDGYALRMPALDQVEEQAIHVSIRPEEFIKDE-----
                                                                                                                                                                                                                                              70;
                                                                                                                                                                                                                                            Score 651.5; DB 2
Pred. No. 1.4e-53;
0; Mismatches 106
                                        -mpv---ekdqklqvllrpedivieeldeneh
                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                              106;
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                                                                                                                                                                                                                                                                Length 381;
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RESULT AAB96796
ID AAB96796
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Matches 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: This patent is in the same patent family as WO200065062, contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                     \verb|mvevrlen|| tkk fgnftavnkln|| tikdgeflv|| lgpsgcgkttt|| rmiagleeptegki||
                                                                                                                                                                                                                                                                                                                                                                                                                                   MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
                                               PANLEKRSDGAYIVFSDGYALRMP----ALDQVEEQAIHVSIRPEEFIKDESGDIEGT-
                                                                                         qklkvttiyvthdqveamtmgdriavmnrgqllqvgpptevylkpnsvfvatfigapem-
                                                                                                                                                                                        lqieelldrypaqlsggqrqrvavaraivvepdvllmdeplsnldaklrvamraeikklq
--nivevsvgdgylegkgfkielpqdimellrdyigktvlfgirpehm-----tvegvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Pages 1569-1570; 1657pp; French
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J, Saurin
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Pred. No. 1.5e-53;
9; Mismatches 129;
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Best Local Similarity
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Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                               Claim 7; Pages 719-720; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                      New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                               Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999;
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                                                                                          YFDDTKINNME-----PSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQT
                                                                           \verb|maevklinvwkkfgdftavkelsleikdgeflvllgpsgcgktttlrmiagleeptiggiangle.|
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yiddklvadpekgifvppkerdvamvfqsyalyphmtvydniafplklrkvpkqeidrrv
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J, Saurin
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
27-NOV-2000;
                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
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                                                                                                                                                                                                                                                             Haemophilus influenzae; otitis media; meningitis
Essential baidentifying
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Local Similarity 39.7%;
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Pred. No. 2.1e-52
4; Mismatches 11
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Best Local
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ARF94410 to AAF94416 represent PCR primers used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                           Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                            Hyperthermophilic archaeon; hyperthermophilic protein
                                                                                                                                                                                                                                                                                                                                                                                                                              Putative P. abyssi ATPase subunit of ABC transporter #7
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  Forterre P,
                                                 (CNRS ) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EX
                                                                                                                             21-APR-1999;
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  Thierry JC,
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  Prieur D,
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Pred. No. 2.1e-51;
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  Dietrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: This patent is in the same patent family as WO200065062, contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Pages 883-884; 1657pp; French.
         09-NOV-2000; 2000WO-US30782
                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                       03-SEP-2001
                                                                                                                                                                                                                         AAG82000 standard; Protein; 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                  17-MAY-2001.
                                                         WO200134809-A2
                                                                                 Staphylococcus
                                                                                                          vaccination;
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                                                                                                          endocarditis.
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                                                                                  epidermidis
                                                                                                                                              open reading frame protein sequence SEQ
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41.9%; Pred. No. 3.3e-51;
62. Mismatches 91;
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                                                                                                                                                ID NO:1094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC (I) and (II) can have antibacterial activity and therefore can be used CC in vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the CC containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be comply to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and therefore identify compounds that may be used for the cartivity and the becompounds that may be 
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                         AAB86541;
                                                               AAB86541 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly WJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQIAQYA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFDDTKI 67
                                                                                                                                                                                                                                                                          ---dfvvniygqnfdcvdmgikenkkvevvirpedislvsqndglfkakvdsmlfrgvhy
                                                                                                                                                                                                                                                                                                                  SDGAYIVFSDGYALRMPALDQVEEQAIHVSIRPEE--FIKDESGDIEGTIRDSVYLGLNT 305
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DB; AAH52850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131;
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Pred. No. 6e-51;
72; Mismatches 1
                                                                                                                                                                                   -stkkanvgsevg
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel recombinant nucleic acid molecule (I), comprising regulatory sequences of a plant cell-active promoter, operatively linked to a DNA sequence encoding a protein with palatinase and/or trehalulase activity, and to plant cell regulatory sequences for transcription termination and/or polyadenylation signal. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription termination and/or polyadenylation signal. The invention used as a selection marker, particularly for transformed plant cells microorganisms. This sequence represents the Erwinia rhapontici ATP-binding protein PalK which is described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palatinase; regulatory region; cell-active promoter; selection marker; plant; ATP-binding protein; palK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. rhapontici
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 42-43; 60pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acids encoding a palatinase or a trehalulase and also comprising plant transcription regulatory sequences are use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH48815, AAH48816
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                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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                                                                                                         qceyqgevmfveqmgnetllyldngnagepwvvrhaersa----ihvgqtvgvrlpvecc
                                                      nlipatlrrsgeqqsvveldngktlvlsiatpa--eaegrsvnigirpehi---rsgnve
                                                                                  NIIPANLEKRSDGAYIVFSDG-----YALRMPALDQVEEQAIHVSIRPEEFIKDESGDIE 292
                                                                                                                                                                                            LMQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREI 179
                                                                                                                                                                                                                                                 FYFDDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLE
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                         ----GTIRDSVYLGLNTDYFIETGFASK---IQVSEESTFEEDLQKGNRIRLRINTQKL
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                                                                                                                                                                                                                                                                                                                                             Score 620.5; DB 2
Pred. No. 1.2e-50;
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Best Local S
Matches 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUL-1998;
19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                           A-QYADRKPDKLSGGQQQRVTLACALAVNPSYLLMDEPLSNLEAKLRLDMRQAIREIQHE 182
sdqqlqrnvselsggqqqrvalaralvlepkilcldeplsnldaklrvdlrkelkrlqke
                                                                                                               DTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQI 123
                                                                                                                                                                                                                               IKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 87; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0125164.
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                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                     Score 617.5; DB 21; Pred. No. 2e-50;
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                                                                                                                                                                                                                                                                                                                                                         107;
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pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as
                                                                                                                                                                                     polypeptides. The proteins and their associated DNA sequences are the treatment, prevention and diagnosis of medical conditions cape, acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usef treating acne vulgaris -
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                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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No. 4.5e-50;
                                                                                                                                                               Skinner
                                                                                                                                                          ΜĂ,
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This represents a Mycobacterium vaccae pota homologue that is homologou to E. coli pota protein. The invention provides M. vaccae polypeptides that comprise an immunogenic portion of a soluble M. vaccae antigen, or a variant, where the antigen induces an immune response in patients previously exposed to a mycobacterium. Such M. vaccae polypeptides can be used in methods for enhancing non-specific immune response. The methods and products can be used for the detection, treatment and prevention of infectious diseases caused by mycobacteria such as M. vaccae, M. avium or M. tuberculosis. The products also have the ability to induce cell proliferation and cytokine production (e.g. interferon-gamma and interleukin-12 production) in T cells, NK cells, B cells, or macrophages. They can be used for enhancing immune responses for use in vaccines or immunotherapy of infectious diseases
Sequence
                                               and cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV34595
                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response enhancers
                                                                                                                                                                                                                                                                                                                                                                                    8; Pages 103-104; 153pp; English
  376
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention of mycobacteria infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              develop products for use
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                                                                        ctgrsnrdyveidvlgstlkarpgettiepgghatlmvrperirvtpgsqdaptgdvacv
                                                                                                           LEKRSDGAYIVFSD-GYALRMPALDQVEEQAIHVS--IRPEEF----IKD-ESGD---I
                                                                                                                                               GITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNIIPAN
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                                       EGTIRDSVYLG
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Qy

В Š Ъ Qy

Matches Query Match Best Local

132;

Conservative

61;

106;

12;

Gaps

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Similarity

33.1%;

Score 610; DB 19; Pred. No. 1.2e-49; Mismatches

Length Indels

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RESULT 1
AAY14879
                AAY14879 standard;
AAY14879;
                                13
                protein;
                376
                B
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밁 Ω В δÃ 망 δÃ 밁

M. vaccae pota gene homologue amino acid sequence

25-OCT-1999

(first entry)

respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous Mycobacterium vaccae protein; antigen; T cell activation; dendritic cell maturation; infectious disease; immune disorder; cell carcinoma; melanoma cytokine; cancer;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Matches 132;
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23-DEC-1997;
23-DEC-1997;
23-DEC-1997;
23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides heat-killed Mycobacterium vaccae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, alopecia areata, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15;
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ratvtdltfqg
                                                                                                          1999-430163/36
                            EGTIRDSVYLG
                                                       ctgrsnrdyveidvlgstlkarpgettiepgghatlmvrperirvtpgsqdaptgdvacv
                                                                                  LEKRSDGAYIVFSD-GYALRMPALDQVEEQAIHVS--IRPEEF----IKD-ESGD---I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response
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                                                                                                                                                                                                                                                                                                                                               Conservative
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97US-0997080.
97US-0997362.
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                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                            Score 610; DB 20; I
Pred. No. 1.2e-49;
Pred. Mismatches 106;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcal protein, useful as a vaccine, for diagnosis pneumococcal diseases and for screening agents capable of anterior inhighting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1998;
19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumococcal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity nes 128; Conserv
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EVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNIIP
                                                                                QIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQH
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                                                                                                                                                                                                                                                                                                               MICROBIAL TECHNICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 605; DB 21;
Pred. No. 3.8e-49;
57; Mismatches 100;
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meningitis; i
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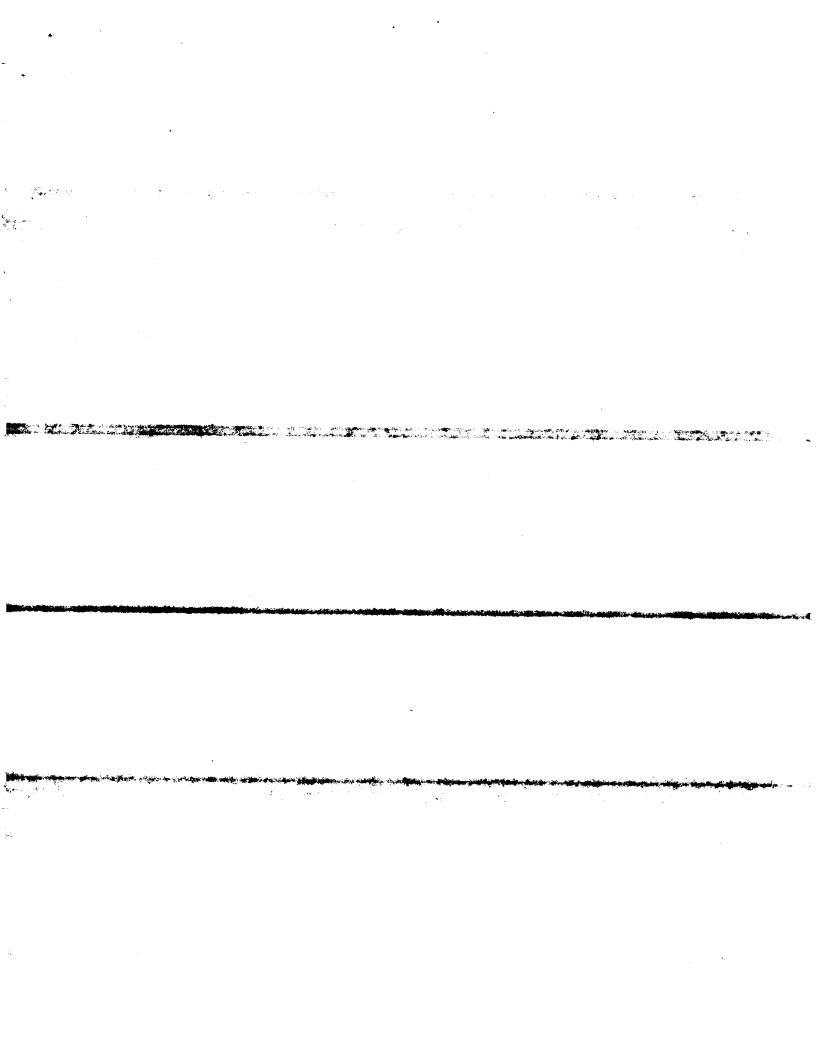
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                                                Best Local Similarity 36.5 Matches 139; Conservative
                                                                                                     Query Match
                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa
Tateishi
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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PVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFDDTKINNMEPSKRN 76
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2000JP-0159162.
2000JP-0280988.
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senoh A, Ikeda
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da M, Oz
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                                                Score 594.5; DB 22,
Pred. No. 4.2e-48;
2; Mismatches 133;
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Ozaki A;
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agdkvhvvaapkdvhlfdgld 389
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                                                        adsmvyvlasgvknpntdllge-gipedmrvtvvgaeetd-----karlgirverhhglk 368
                                                                                                                                FSDGYALRMP-----ALDQVEEQAIHVSIRPEEF---IKDESGDIEGTIRDSVYLG
                                                                                                                                                                                      AMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIG--RTNIIPANLEKRSDGAYIV 254
                                                                                                                                                                                                                                  gqrqrvamgraivrepsvfcmdeplsnldaklrvstraeisglqrrmgvttvyvthdqve
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Search completed: July 30, 2002, 15:47:43
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1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
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US-08-469-617-36
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US-08-8898-779-3
US-09-224-502-4
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US-09-426-1083-30
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US-09-88-88-2073-33-30
US-09-88-88-3073-33-30
US-08-784-6494-2
US-08-583-276-19
US-08-583-276-19
  US-08-858-207A-332
US-08-665-259-25
US-08-762-500-25
US-08-762-500-75
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Sequence 89, Appl
Sequence 89, Appl
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Sequence 6, Appl
Sequence 13, Appl
Sequence 315, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 2, Appli
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Sequence 27, Appli
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Sequence 29, Appli
Sequence 25, Appli
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US-08-997-080-89
         Query Match
Best Local Similarity
Matches 132; Conserv
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Patent No. 5968524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WATSON, JAMES D. APPLICANT: TAN, PAUL L.J. TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2601 F
                                                                                                                                                                  TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                   USA
              Conservative
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ALIGNMENTS

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INFORMATION FOR SEQ ID NO: 89
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-080-89
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/997,080 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
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33.1%; Score 610; DB 2; 42.4%; Pred. No. 2.6e-55;

Length 376; Indels

12;

Gaps

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61;

Mismatches

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US-08-997-362-89
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                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELEPHONE: 206-269-0565
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                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICANT: Scott, Linc
APPLICANT: Prestidge,
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LENGTH: 376 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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GADVSRTPPNKRNVNTVFQHYALFPHMTVWDNVAYGPRSKKLGKGEVRKRVDELLEIVRL 121
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5985287
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2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Visser, Elizabeth
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                                                                                                                                                                                                                                     No.
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                                                                                                                                                                                                                                     5985287 08/705,347
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; TOPOLOGY: 1i; MOLECULE TYPE: US-08-997-362-89
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US-08-873-970-89
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                      ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 LEKRSDGAYIVFSD-GYALRMPALDQVEEQAIHVS--IRPEEF----IKD-ESGD---I 291
                                                                                                                   APPLICATION NUMBER: 08/7 FILING DATE: 29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2601 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEFAERRPAQLSGGQQQRVALARALVNYPSALLLDEPLGALDLKLRHVMQFELKRIQREV
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o. 6001361
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                                          11000.1002C1
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Pred. No. 2.6e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 n W. Speckman
Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF,
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TELEFAX:

206-269-0563

FILING DATE:

12-JUN-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 89, App...
                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6160093
GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compounds TITLE OF INVENTION: Treatment NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                COUNTRY: (ZIP: 9812)
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                                                                                                                                                                                                                                                                 CITY:
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                                                                                                                                                                                                                                                              Seattle
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Skinner, Margot
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; ORGANISM: Mycobacterium vaccae US-09-324-542-89
                                                                                                                                                                                                                                                                                                                                                                                   US-09-324-542-89
                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Sequence 89, Application US/09324542 Patent No. 6328978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 132;
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Best Local Similarity
                                                                                                                         APPLICANT: Watson, James D.
APPLICANT: Watson, Paul L.J.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                     TYPE: PRT
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TELECOMMUNICATION INFORMATION: 206-269-0565
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
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23-DEC-1997
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                                                                                           Windows Version
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Pred. No. 2.6e-55;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 30-AUG-1993
                                                                                                                                      APPLICATION NUMBER: US 07/986,928 FILING DATE: 08-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                REGISTRATION NUMBER: 30,944
REFERENCE/DOCKET NUMBER: P/1261-13
TELECOMMUNICATION INFORMATION:
                                                                   APPLICATION NUMBER: US 07/612,330 FILING DATE: 13-NOV-1990 ATTORNEY/AGENT INFORMATION: NAME: Gray III, William O.
                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 27-AUG-1993
                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: OSTROLENK, FABER, GERB & SOFFEN 1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pei, Zhiheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blaser, Martin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.1%;
                                                                                                                                                                                                                         US 08/112,387
                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version
                                                                                                                                                                                                                                                             US 08/114,420
                                                                                                                                                                                                                                                                                                                                US/08/402,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 610; DB 4;
Pred. No. 2.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                     #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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US-08-919-573-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO:
                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                    REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Bloom, Allen
                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 QHEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 99, L. CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SHQSNTTMVVVTHEMGFAKEVADRIIFMEDGAIVEENIPSEFFSNPKTERARLFLGK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VVGLLDKANVYPATLSGGQQQRVAIARSLCTKKPYILFDEPTSALDPETIQEVLDVMKEI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LMQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREI 179
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 242 amino acid
                                                                                                       TELEFAX:
                                                                                                                                                                     REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NLVLNHKNKIEICRKYCAMVFQHFNLYPHMTVLQNLTLAPMKLQKKSKKEAEETAFKYLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
STRANDEDNESS:
                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IELKNVNKYYGTHHVLKIFNLSVKEGEKLVIIGPSGSGKSTTIRCMNGLEEVSSGEVVVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                                                                                                                                                        08543
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                  amino acid
                                  244 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       997 Lenox Drive, Building 3, Suite
                                                                                                       609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burnham,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dechert Price
                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
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31.6%;
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NOVEL GLUTAMINE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-BINDING PROTEIN 6
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                                                                                                                                                        P50597
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Pred. No. 2.2e-28;
5; Mismatches 103
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Query Match
Best Local Similarity
Thes 75; Conserve
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                                                                                                                US-08-919-573-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08919573 Patent No. 6346392
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APPLICANT: Burnham,
TITLE OF INVENTION:
                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: P55
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 LA-KSGMTMVIVTHEMGFAREVADRVIFMADGVVVVEDGTPEQIFEQTQEQRTKDFLSK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 IQHEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 EKVGLPDKADAYPQSLSGGQQQRIAIARGLAMEPDVLLFDEPTSALDPEMVGEVLAVMQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ELMQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIRE 178
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nes 75; Conserv
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                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                            TELEFAX: 609-520-3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GVDITDKKNDLFAMREKMGMVFQQFNLFPNMTVIENITLSPIKTKGESREVAEKRAQKLL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DTKI----NNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQ-QTNKYL 118
                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 IKIENLHKSFGKNEVLKGINLEIKRGEVVVIIGPSGSGKSTLLRSMNLLEEATKGKVIFE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 IKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08543
                                                                                                                                                                  amino acid
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997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                   244 amino acids
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                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
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                                                                                                                                                single
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31.5%; Pred. No. 5.7e-28;
ative 59; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martin, Karl Russel
NOVEL GLUTAMINE TRANSPORT
ATP-BINDING PROTEIN
                 18.7%; Score 345; DB 4; Length 244; 31.5%; Pred. No. 5.7e-28; ive 59; Mismatches 98; Indels
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                                                                                                                                                                                                                          4:
                                                                                                                                                                                                                                                                                                                    P50597
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                   6
                 Gaps
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; MOLECULE TYPE: US-08-858-207A-315
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          Matches
                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nicholas, ....
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
TITLE OF TOTAL STORY ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-MAY-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LA-KSGMTMVIVTHEMGFAREVADRVIFMADGVVVEDGTPEQIFEQTQEQRTKDFLSK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 EKVGLPDKADAYPQSLSGGQQQRIAIARGLAMEPDVLLFDEPTSALDPEMVGEVLAVMQD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 IQHEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGR 236
                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 709 Sweaerand
CITY: King of Prussia
                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Disl
COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 GVDITDKKNDLFAMREKMGMVFQQFNLFPNMTVIENITLSPIKTKGESREVAEKRAQKLL 125
                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELMQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIRE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTKI----NNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQ-QTNKYL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKIENLHKSFGKNEVLKGINLEIKRGEVVVIIGPSGSGKSTLLRSMNLLEEATKGKVIFE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315, Application US/08858207A
5. 6348328
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       l Similarity
72; Conserv
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                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                         203 amino acids
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Knowles, David
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black, Michael
                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                       No. 6348328e
                                                                                                                                                                                                                                                                          single
                                      18.4%;
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57; Mismatches
                                   Score 338.5; DB Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P50475
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                                                                  DB 4;
       69;
       Indels
                                                                      Length
                                                                      . 203;
       5.
   Gaps
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1 MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF 60

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US-08-466-886-36
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                                                                                                                    Matches
                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,886
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329.0010006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Buckwald TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 -NRELGMTQIVVTHDLQFAENIA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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STRANDEDNESS:
TOPOLOGY: not
                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                  1 KAWGEVVVSKDINIDIHEGEFVVFVGPSGCGKSTLLRMIAG------ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQLGLGGHAESYPFSLSGGQKQRVALARAMMIDPEIIGYDEPTSALDPELRLEVEKLILQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELMQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIRE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFDDTKINNMEPSKRN-IGMVFQNYAIFPHLIVRDNVAFGLMQKK-VPKEELIQQTNKYL 118 :: : : | | :: : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYNGQPLELDELQKRNLLGFVFQDFQLFPHLSVLENLTLSPVKTMGMKQEEAEKKASGLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLELRNIN--KVFGDKQILSDFSLSIPEKQILAIVGPSGGSKTTLLRMLAGLETIDSGQI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20005
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Collins, Francis S.
Iannuzzi, Michael C.
Drumm, Mitchell L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buckwald, Manuel
VENTION: Cystic Fibrosis Gene
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riordan, John R.
Rommens, Johanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsui, Lap-Chee
                                                                                                                                                                                                                                     SS: not relevant not relevant
                                                                                                                                                                                                                   peptide
                                                                                                               15.9%; score 293.5; DB 1; 40.0%; Pred. No. 3.8e-23; ative 22; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/466,886
                                                                                                                                                 Length 111;
                                                                                                                  Indels
                                                                                                                  49;
                                                                                                                Gaps
                                                                                                                  <u>ب</u>
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	QY 131 PDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRL 170 	
	Qy 71 EPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQIAQYADRK 130 : : : : : bb 42VGMVFQSYALVPHLSVAENMSFGL	
	Qy 11 KIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFDDTKINNM 70 : : :: :	
2	Query Match 15.9%; Score 293.5; DB 4; Length 111; Best Local Similarity 40.0%; Pred. No. 3.8e-23; Matches 64; Conservative 22; Mismatches 25; Indels 49; Gaps	
	t rele pepti	_
	LENGTH: TYPE:	
	INFORMATION FOR SEQ ID NO: 36:	
	TELEPHONE COLLEGE 100 TELEPHONE 202-371-2600	
	REFERENCE/DOCKET NUMBER: 1329.0010008 TELECOMMINITATION INFORMATION:	
	tein, Jorg	
	, S	
	; APPLICATION NUMBER US/08/469,617 : FILING DATE: 06-JUN-1995	
	IBM PC	
	ER READABLE FORM	
	S	
	; CITY: Washington ; STATE: DC	
	•• 02	
	CE ADDRESS:	
	3 17	
	APPLICANT: Drumm, Mitchell L. ADDITCANT: Burkwald Manual	
	; APPLICANT: Rommens, Johanna M. ; APPLICANT: Kerem, Bat-Sheva	
	: Riordan, John R.	
	FRICEIL NO. OXULLU; GENERAL INFORMATION: - APPLICANT: TSUI LAD-Chee	
	9-617 ce 36	
	Db 72 PKALSGGRQQRVAIGRTLVAEPSVFLLDEPLSNLDAALRV 111	
	Qy 131 PDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRL 170	_
	Db 42KPADRK 71	

RESULT

Michael Arthur

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                              Sequence 4, Application US/08898779 Patent No. 5882891
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                       Matches
                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burnham, Martin, Karl Russel
APPLICANT: Lonetto, Michael Arthur
APPLICANT: Warren, Patrick Vernon
TITLE OF INVENTION: NOVEL Ferrichrome transport
TITLE OF INVENTION: ATP-Binding Protein
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                              133
                                                                                                                                                              187
                                                                                                                              193 IVMVLHDINQAIRFSDHLIAMKEGDIIATGSTEDV 227
                                                                                                                                                                                                                                                        73 KEIAKKIAILPQSPEVADGLTVGELVSYGRFPHQKGFGRLTAEDKKEIDWAMEVTGTDTF 132
                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                    13 YHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFDDTKINNMEP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                           TVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKEL 221
                                                                                                                                                                                          RHRSINDLSGGQRQRVWIAMALAQRTDIIFLDEPTTYLDICHQLEILELVQKLNQEQGCT
                                                                                                                                                                                                                          ADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQHEVGIT 186
                                                                                                                                                                                                                                                                                    SK--RNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLE-LMQIA---QY 126
                                                                                                                                                                                                                                                                                                                      YGDNTIINKLDVEIPDGKVTSIIGPNGCGKSTLLKALSRLLAVKEGEVFLDGENIHTQST 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                       62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08898779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
 Burnham, Martin, Karl Russel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 271; DB 2; L
28.8%; Pred. No. 3.4e-20;
cc. Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/898,779
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 265;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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NUMBER OF SEQUENCES:
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; Sequence 2, Application US/09224502
; Patent No. 6264955
; GENERAL INFORMATION:
APPLICANT: Burnham, Martin, Karl
APPLICANT: Lonetto, Michael Arthu
APPLICANT: Warren, Patrick Vernon
APPLICANT: Warren, VOYEL Ferrich
TITLE OF INVENTION: ATP-Binding P
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ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3,
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 14.7%; Score 271; DB 2; 1 Similarity 28.8%; Pred. No. 3.4e-20; 62; Conservative 56; Mismatches 91;
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                     , Michael Arthur
Patrick Vernon
NOVEL Ferrichrome transport
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NOVEL Ferrichrome transport
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                                                                                           Karl Russel
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Dechert Price 997 Lenox Drive,

& Rhoads Building 3,

Suite

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RESULT 15
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Best Local Similarity
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                                                                                                        APPLICANT: Burnham, Martin, Karl Russel
APPLICANT: Lonetto, Michael Arthur
APPLICANT: Warren, Patrick Vernon
TITLE OF INVENTION: NOVEL Ferrichrome transport
TITLE OF INVENTION: ATP-Binding Protein
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REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                     NUMBER OF SEQUENCES: 4
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MEDIUM TYPE: Diskett
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                              ADDRESSEE: Dechert Price & Rhoads STREET: 997 Lenox Drive, Building 3, Suite 210
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Pred. No. 3.4e-20;
56: Mismatches 91;
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 265 amino acids
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 193
                       187 TVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKEL
                                                         133 RHRSINDLSGGQRQRVWIAMALAQRTDIIFLDEPTTYLDICHQLEILELVQKLNQEQGCT 192
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                                                                                                                                                73 SK--RNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLE-LMQIA---QY 126
                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                                                     ADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQHEVGIT 186
                                                                                                                    KEIAKKIAILPQSPEVADGLTVGELVSYGRFPHQKGFGRLTAEDKKEIDWAMEVTGTDTF 132
IVMVLHDINQAIRFSDHLIAMKEGDIIATGSTEDV
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Pred. No. 3.4e-20;
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Perfect score:
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ALIGNMENTS

A.Status: preliminary
A; Molecule type: DNA
A; Residues: 1-363 < KUR> C; Geneti A; Gene: C; Accession: D95028

C; Accession: D95028

R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

Sc RESULT 1

D95028
ABC transporter, ATP-binding protein SP0242 [imported] - Streptococcus pneumoniae (st C;Species: Streptococcus pneumoniae
C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 B Š QV В δÕ В δÃ В A;Cross-references: GB:AE005672; PIDN:AAK74421.1; PID:g14971711; GSPDB:GN00164; TIGRA; Experimental source: strain TIGR4 Š Вb Qy Вþ Qy A, Experimental source: Query Match Best Local S Matches 363 Genetics: 301 301 241 241 181 121 181 121 61 61 Local Similarity les 363; Conserv SP0242 PANLEKRSDGAYIVFSDGYALRMPALDQVEEQAIHVSIRPEEFIKDESGDIEGTIKDSVY HEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNII MQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQ LGLNTDYF1ETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNLIKGVN HGT 363 LGLNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNLIKGVN PANLEKRSDGAYIVFSDGYALRMPALDQVEEQAIHVSIRPEEFIKDESGDIEGTIRDSVY HEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNII MQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQ Conservative 100.0%; Score 1843; DB 2; 100.0%; Pred. No. 2.9e-122; tive 0; Mismatches 0; #text_change 03-Aug-2001 Length 363; 0; Gaps 300 300 180 180 120 120 60 60 240 0

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ster, E.W.
A;Title: Th
                                                          hypothetical protein Atu4578 [imported] - Agrobacterium tumefaciens (strain C: C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C; Accession: AF3119 R; Wood, D:W; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6) C.Species: Streptococcus pneumoniae c.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C.Accession: F97899 C.Accession: F97899 C.Accession: F97899 C.Accession: J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B. R.; Boskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, P.; Sun, P.M.; Winklet, M.E. J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winklet, M.E. J.; Lu, J.; Matsushima, P.; McAhren, J. Bacteriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A.; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A.; Reference number: A97872; MUID:21429245; PMID:11544234
A.; Accession: F97899
A. Status: preliminary A.; Accession: P97872; MUID:21429245; PMID:11544234
A.; Accession: P97872; MUID:21429245; PMID:11544234
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Natural Genetic; PMID:11743193
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A;Accession: AF3119
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: DNA
A;Residues: 1-365 <KUR>
A;Residues: 1-365 <KUR>
A;Cross references: GB:AE008689; PIDN:AAL45372.1; PID:g17743068; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.1
300
                                     293
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                                   GTIRDSVYLG--LNTDYFIETGFASK------IQVSEESTF
                                                                        TLD----RTGGQTSISS--LKVTLPQADAISKDRTIVAAIRPEAISIGPSIGNCDERIELP
                                                                                                       PANLEKRSDGAYIVFSDGYALRMPALDQV-EEQAIHVSIRPEEFI------KDESGDIE
                                                                                                                                                                 MQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQ
                                                                                                                                                                                                                                                                                                  SIERQAIEHVPAHKRDVGMVFQDYAVFPHISVFDNIAFGLKQRKSSSAEIRERVGKILDV
                                                                                                                                                                                                                                                                                                                     YFDDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLEL 120
                                                                                                                                                                                                                                                                                                                                                                          MAAVEITSIKKSYRDVVALSDINISIPSGSFFTLLGPSGCGKTTLLRTIAGFHQQDSGSI
                                                                                                                                                                                                                                                                                                                                                                                             MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
VTIRQVSFTGREMNVAAVLSSGEEIEAITKPSPEIIALQPNQKTTF
                                                                                                                                              QAMNITTYYYTHDQEEALAMSDLVCVMYGGVIQQAAPPWEVYNNPANRFVASFVGANNFL
                                                                                                                                                                                                                        VQLAPYAKRMPHELSGGQQQRVGLARALVINPKVLLMDEPLSNLDAKLRVDLRRELREIQ
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45.1%;
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Pred. No. 5e-44;
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345
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hypothetical protein AGR_L_589 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 A; Gene: AGR_L_589 A; Map position: 1 C; Genetics: A; Cross-references: GB: AE007870; A; Molecule type: DNA A; Residues: 1-374 < KUR> A; Status: preliminary A;Title: Genome Sequence of the Plant Pathogen and A;Reference number: A97359; PMID:11743194 A;Accession: A98168 R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001 C; Accession: A98168 A98168 Query Match
Best Local Similarity
Matches 156; Conserv 61 74 14 1 MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF SIERQAIEHVPAHKRDVGMVFQDYAVFPHISVFDNIAFGLKQRKSSSAEIRERVGKILDV YFDDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLEL 120 MAAVEITSIKKSYRDVVALSDINISIPSGSFFTLLGPSGCGKTTLLRTIAGFHQQDSGSI linear chromosome Conservative 39.7%; 45.1%; 66; PIDN:AAK88867.1; PID:g15158633; GSPDB:GN00170 Score 731; DB 2; Pred. No. 5.2e-44; S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.; Mismatches <u>ب</u> 98; Biotechnology Agent Agrobacterium Length 374; Indels 26; Gaps 60 B.; Gold Markelz, 6 C58, Goldm

G

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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUID:99287316
A;Refession: A72279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <ARN>
A;Residues: 1-355 <ARN>
A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36307.1; PID:g498178
C;Genetics:
C;Genetics:
A;Gene: TM1232
C;Superfamily: inner membrane protein malk; ATP-binding cassette homology
F;19-210/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sugar ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C:Accession: A72279
C:Melson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.
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A72261
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                                                                                                                                                                                                                                                                                                                                                                                                              SVYLG--LNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNL
                                                                                                                                                                                                      PANLEKRSDGAYIVFSDGYALRMPALDQVEEQAIHVSIRPEEFIKDESGD---IEGTIRD
                                                                                                                                                                                                                                                             MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTIRQVSFTGREMNVAAVLSSGEEIEAITKPSPEIIALQPNQKTTF
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                                                                                             EVYFAEKLMSDTILHLNVGSE-KIVAKIPGDVDFRSGEKITFFLDVEKIHLFHPETGERI
                                                                                                                                                                     FLEMEVRSEGNSVVLQNG-EIKIPAKTDPGAKKVILGIRPENVYLEEKPNTLKLEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAQVKIDGVKKYFGNVRALDGIDLVVNEGEFLVLLGPSGCGKTTLLRCIAGLEQVTGGKI
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                                                                                                                                                                                                                                          ERIGVTTIYVTHDQTEAMTMGDRIAVMNQGKLQQVGTPSEIYHHPVNIFVAGFVGSPQMN
                                                                                                                                                                                                                                                                                                                     LHISELLDRYPAQLSGGQRQRVAVARAIVHEPEVLLMDEPLSNLDALLRVKMRSELKKLQ
                                                                                                                                                                                                                                                                                                                                                                                             FFNDRDVTNLPPKDRNISMVFQSYAVWPHMKVYDNIAYPLKLKKVPKEE1EKRVKWAADL
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     ABC
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   transporter,
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   ATP-binding
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   protein
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   Thermotoga
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C:Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_r C;Accession: A72261 R;Nelson, K.E.; Clayton, R.A.; Garrett, M.M.; Stewart, A.M.; C
                                                                                                                                                                                                                                            ABC transporter, ATP-binding protein VCA0602 [imported] - C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_c C;Accession: H97617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Evidence for lateral gene transfer A; Reference number: A72200; MUID:99287316
                                                                                                                               A;Title: Genome Sequence of the Plant Pathogen and A;Reference number: A97359; PMID:11743194 A;Accession: H97617
                                                                                                                                                                                                       R; Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger,
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A;Experimental source: strain MSB8
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                                                                         A; Molecule type: DNA
A; Residues: 1-352 < KUR>
                                                                                                                                                                                         Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                   C; Genetics:
                                                       A; Cross-references:
                                                                                                             A; Status: preliminary
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Best Local
position:
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                 AGR_C_3896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEEHAQKMPSQLSGGQKQRVAIARALANEPRVLLLDEPLSALDAKLRQELLVELDNLHDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVVEVEDEYYVVESPGIGQFRCYRDKEAKKGDRLLITLRPEKIRISRKQFRSEETFNVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGITFIYVTHDQAEAISVSDRVALMNEGEIVQVGTPYEVYESPVNVFAATFIGETNLMKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVSIKNVSKFFDDFQVLKNVSLDIKKGEFFSILGPSGCGKTTLLRVIAGFEGVESGDVLL
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                                                       GB:AE007869;
chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%;
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Cotton, M.D.; Pratt, M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                       PIDN: AAK87897.1;
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Pred. No. 6.5e-42;
5; Mismatches 102
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homology
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                                                                                                                                                                                                       Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
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                                                       PID:g15157291; GSPDB:GN00169
                                                                                                                                                                     Biotechnology
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; Phillips, C.A.;
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                                                                                                                                                                   Agent Agrobacterium
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A.; Richardson,
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Query Match Best Local Similarity

36.4%; 44.1%;

Score Pred.

671; DB 2; No. 7.9e-40;

Length

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ster, E.W.

A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; PMID:11743193
A;Accession: AF2840
A;Accession: AF2840
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; McLecule type: DNA
A; Residues: 1-352 < KUR>
A; Cross-references: GB:AEO08688; PIDN:AAL43140.1; PID:g17740615; GSPDB:GN00186
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AF2840
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wooderstee, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Atu2150 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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Best Local S
Matches 146
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PANLEKRSDGAYIVFSDGYALRMPALDQVEEQAIHVSIRPE--EFIKDESGD--IEGTIR
                                                                                                                            MQIAQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQ
                                                                                                                                                                      VINGKDQTTLRPNQRNIGMVFQAYALFPNMNVYENVAFGLKVAGKPKAEIDARVKEMLQL
                                                                                                                                                                                                                                                        MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
                                   QKLGITTIFVTHDQEEALSISDRIVVMNGGRADQIGSPFDIYNKPATRFVASFVGTLNLI
                                                                 HEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNII 240
                                                                                                                                                                                          YFDDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLEL
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                                                                                                     IHLEHLADRYPYQMSGGQQQRVALARALAPKPEVLLLDEPLSALDAKIRVSLREEIRQIQ
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146; Conser
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                                                                                                                                                                                                                                                                                                                             36.4%;
44.1%;
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                                                                                                                                                                                                                                                                                                                         Score 671; DB 2; Pred. No. 7.9e-40;
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                                                                                                                                                                                                                                                                                                         113;
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K awa, H.; Takamiya, M.; Masudá, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 199
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
A;Accession: H72555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transporter ATP-binding protein APE1732 - C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 C;Accession: H72555
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A;Residues: 1-358 <KAW>
A;Residues: 1-358 <KAW>
A;Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80733.1;
A;Experimental source: strain K1
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YRQAGS
                                  FSADGS 352
                                                                     FEGKVSLAMFLGWRTQLKVEVG
                                                                                                    IEGTIRDSVYLGLNTDYFIETGFASKIQVSEESTFEEDLQK----GNRIRLRINTQKLNI 346
                                                                                                                                       DGRVSEVLGSGMVRVALEG-GLSIVGTDMEGGLRQGERVKVVIRPER-VKVGHEYNGENV
                                                                                                                                                                          PANL-EKRSDGAYIVFSDGYALRMPALDQV----EEQAIHVSIRPEEFIK---DESGD--
                                                                                                                                                                                                                                              HEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIGRTNII 240
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n: ATP-binding cassette
   357
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39.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
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Pred. No. 8.8e
76; Mismatches
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homology <ABC>
                                                                     -GQEITIYSDPRRAPLPGQPVRFYIDPEEAKV
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision

A82398

10

maltose/maltodextrin ABC transporter, ATP-binding protein VCA0946 [imported]

20-Aug-2000 #text_change 02-Feb-2001

Vibrio

Gwinn, M.L.; Dodson, R.

C; Accession: A82398

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RESULT 11
B98169
ATP-binding transport protein smoK (polK) AGR_L_604 [imported] - Agrobacterium in C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: B98169
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.;
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Marl
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobactu
A;Reference number: A97359; PMID:11743194
A;Recession: B98169
A;Accession: B98169
A;Accession: B98169
A;Accession: B98169
A;Residues: 1-346 <KUR>
A;Residues: 1-346 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88876.1; PID:g15158643; GSPDB:GN00170
C;Gene: AGR_L_604
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: A8238
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 < HEID>
A;Cross-references: GB:AE004421; GB:AE003853; NID:g9658375; PIDN:AAF96842.1; GSPDB:GN00.
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0946
A;Map position: 2
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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                                                                                         36.2%; Score 666.5; DB 2;
41.4%; Pred. No. 1.6e-39;
tive 64; Mismatches 115;
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Doughty, D.; Scott, C.; Lappas, C.; Markelz,
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TVSAVSFMGANALYTVEIG-GRQIRVS-QSGAETLIDAGQRVALQ
                                                                                                                                                 RRIGATSLYVTHDQAEAMAMSDRIVVMNAGRVVEIGTPLELYRAPKHAFTAGFLGQTNLL
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                                                                                                                                                                                                                                                                                                       RLGGKRIDQAQPEARDIAMVFQSYALFPHMSVAKNLGFGLKMKKVAKDERARRIAHALEI
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VSAEGQQAQLPWGQSVTLDQAAAGNVQISARPENIHICADQAGD--G

286 293 240 240 180 120

329 338

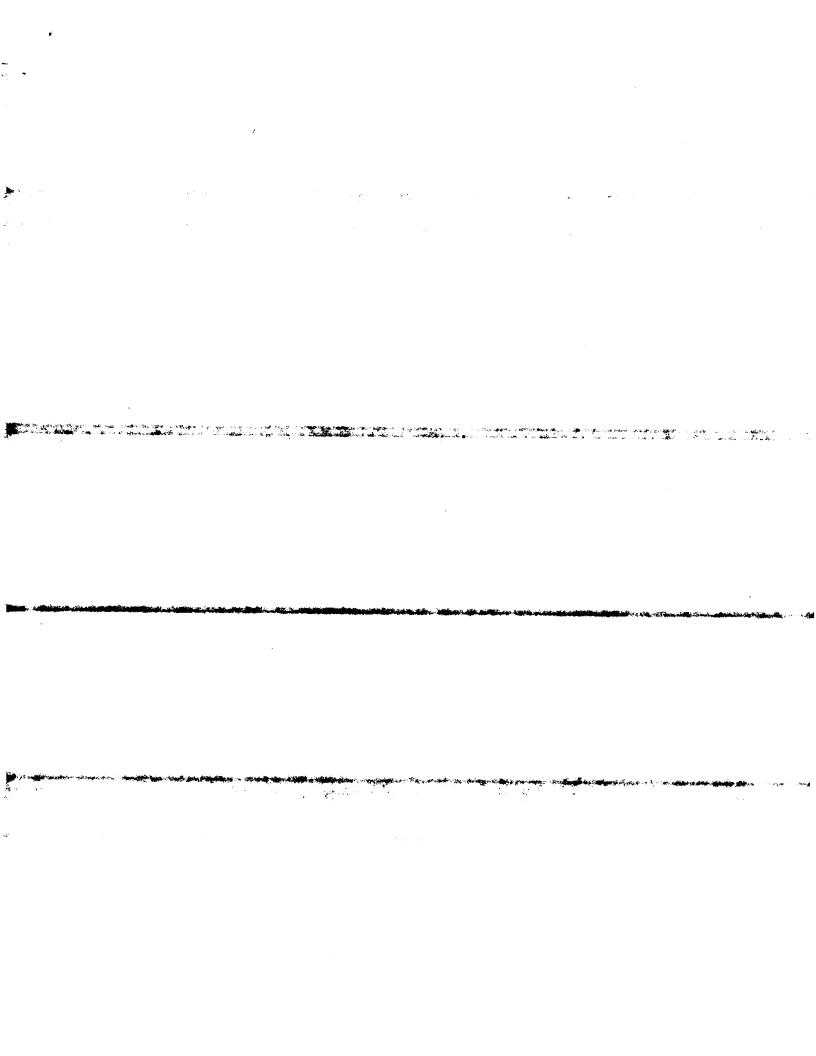
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C;Accession: AE3118
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthmer, D.; Kutyavin, T.; Levy, R.; Li, M.; N.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-346 <KUR>
A; Cross references: GB: AEO08689; PIDN: AAL45363.1;
A; Experimental source: strain C58 (Dupont)
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A;Accession: AE3118
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Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                                                                                                                                      36.2%;
                                                                                                                                                                                                   ; Score 666.5; Db 2,
Pred. No. 1.6e-39;
                                                                                                                                                                                                                                       64;
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glucose ABC transporter ATPase BMEII0593 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3583
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3583
C;Date: 01-Feb-2002
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;Datum, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AH3583
  A; Molecule type: DNA
A; Residues: 1-351 <KUR>
A; Cross-references: GB:
                                                                                               A; Reference number: AD3252;
A; Accession: AD3587
                                                                                                                                         R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
                                                                                                                                                                                                                                         SN-glycerol-3-phosphate transport ATP-binding protein ugpC BMEII0621 [imported] -C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3587
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A; Residues: 1-373 < KUR>
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Best Local S
Matches 150
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les 150; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      -SVFFDSASQTRI
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    GB:AE008918;
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Pred. No. 3.7e-39;
62; Mismatches 141;
    PIDN: AAL53863.1;
PID:g17984801;
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    GSPDB:GN00191
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A;Gene: SCOEDB:SC8B7.10c
C;Superfamily: unassigned
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                                                                                                                                                                                                                                                                                                                                                                                                  probable polyamine ABC-transporter ATP-binding protein -C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_C;Accession: T35802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
C; Genetics:
A; Gene: BMEII0621
A; Map position: II
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A; Residues: 1-397 < M
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                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T35802
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Best Local
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Best Local Similarity 40.2
Matches 148; Conservative
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                                                                                                 EIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYF
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                                                         DDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQ 122
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                                                                                                                                                         Score 661.5; DB 2
Pred. No. 4.4e-39;
6; Mismatches 134
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Pred. No. 3.7e-39;
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Minimum DB
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
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367.5	368	372	375	389	394	412.5	420	421	423	427	431
19.9	20.0	20.2	20.3	21.1	21.4	22.4	22.8	22.8	23.0	23.2	23.4
267	240	308	263	242	242	297	560	400	400	381	380
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Y412_METJA	GLNQ_ECOLI	YEHX_ECOLI	BZTD_RHOCA	GLUA_CORGL	GLNQ_BACST	YD67_METJA	POTA_MYCPN	PROV_SALTY	PROV_ECOLI	OPBA_BACSU	OPCA_BACSU
Q57855 methanococc		P33360 escherichia		P48243 corynebacte					_	Q45460 bacillus su	

ALIGNMENTS

DR DR DR DR DR DR DR DR FT	888888888888	C R R R R R R R R R R R R R R R R R R R	RESULT POTALH AC POTAL AC POTA
sportr. A. RTER; 1. membrane; Complete prot ATP (POTENTIAL). 3E61DD3D062EBECA CRC64	FOR SPERMIDINE/PUTRESCINE. PROBABLY RESPONSIBLE COUPLING TO THE TRANSPORT SYSTEM (BY SIMILARITY SUBCELLULAR LOCATION: Inner membrane-associated SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILS SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are no by non-profit institutions as long as its curve of the swiss statement is not removed. Usage ittes requires a license agreement (See http://wssend an email to license@isb-sib.ch).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=RD / KW20 / ATCC 51907; MEDILNE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb JF., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb JF., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb JF., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb JF., Cocapane J.D., Scott J.D., Shirley R., Liu LI., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 260:496-512(1995).	1 5

Length

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Kimura S., Kitagawa M.
Mori H., Motomura K.,
Sampei G., Seki Y., Ta
Yano M., Horiuchi T.;
"A 718-kb DNA sequence
                                                                                                                                                           SEQUENCE From MG1655;

STRAIN=K12 / MG1655;

MEDLINE=99426617; PubMed=9278503;

MEDLINE=99426617; PubMedt G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode M.A., Rose I
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16-OCT-2001 (Rel. 40, Last annotation update)
Spermidine/putrescine transport ATP-binding protein
POTA OR B1126 OR Z1831 OR ECS1571.
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ECOLI
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Furuchi T., Kashiwagi K., Kobayashi H.,
"Characteristics of the gene for a sperr
transport system that maps at 15 min on
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
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01-NOV-1991 (Rel. 20,
16-OCT-2001 (Rel. 40,
                                                                  Ikemoto
                                                                                Oshima
                                                                                           MEDLINE=97061202; PubMed=8905232;
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                       a T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Co K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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Pred. No. 9.2e-40;
0; Mismatches 106;
  Escherichia
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ETFAQRKPHQLSGGQQQRVAIARAVVNKPRLLLLDESLSALDYKLRKQMQNELKALQRKL

AQYADRKPDKLSGGQQQRVTLACALAVNPSVLLMDEPLSNLEAKLRLDMRQAIREIQHEV

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MEDLING-2115C31; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa C., Ogasawara N., Yasunag Kuhara T., Tahaka M., Tobe 1 Iida T., Tahkani H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."

"Nature 409:529-533(2001).
                                                                                                                                                                                                                             Transport; ATP-binding; Inner membrane; Complete
NP_BIND 50 57 ATP (BY SIMILARITY).
SEQUENCE 378 AA; 43028 MW; 14DCA99329A344F3 C
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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EcoGene; EG10749; potA.
InterPro; IPR003593; AAA.
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InterPro; IPR001687; ATP_GTP_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Inner membrane-associated. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                       IKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFD
                DTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQI: | : : | : : | ::|:: : : | ::|:
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r; SM00382; AAA; 1.
rTE; PS00211; ABC_TRANSPORTER; 1.
                                                                      VQLAGIRKCFDGKEVIPQLDLTINNGEFLTLLGPSGCGKTTVLRLIAGLETVDSGRIMLD
 NEDITHVPAENRYVNTVFQSYALFPHMTVFENVAFGLRMQKTPAAEITPRVMEALRMVQL
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AP002555; BAB34994.1;
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an email to license@isb-sib.ch).
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Pred. No. 3.1e-39;
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M., Tobe T.,
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AFUC_ECOLI STANDAKU;
P37009; P77157;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence up:
16-OCT-2001 (Rel. 40, Last annotation)
16-OCT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                     MEDLINE=94156832; PubMed=8113168;

VOLKert M.R., Loewen P.C., Switala J., Crowley D., Conley M.;

"The delta (argf-lacz)205(U169) deletion greatly enhances resi
to hydrogen peroxide in stationary-phase Escherichia coli.";

J. Bacteriol. 176:1297-1302(1994).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.; "Systematic sequencing of the Escherichia coli genome: analysis of "Systematic sequencing of the Escherichia coli genome: analysis of "0.6.0 min (189,987 - 281,415bp) region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
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                                                                                                      TRANSPORT SYSTEM.

MISCELLANEOUS: IN E.COLI, THE AFU SYSTEM SEEMS TO HAV DELETED BY AN INSERTION SEQUENCE. AFUA IS TOTALLY LOS PARTIALLY PRESENT AND AFUC IS TOTALLY CONSERVED.

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

CAUTION: REF. 4 DIFFERS FROM THAT SHOWN FROM POSITION
                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Matches
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Best Local :
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Q01937;
Q1-APR-1993
Q1-APR-1993
16-OCT-2001
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
PROSTITE; P$00211; ABC_TRANSPORTER; 1.
Iron transport; Transport; ATP-binding; Complete proteome.
NP_BIND 39 46 ATP (POTENTIAL).
CONFLICT 147 148 LA -> WP (IN REF. 2).
SEQUENCE 348 AA; 39059 MW; D4AD33754217DA1A CRC64;
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Williams S.G., Greenwood J.A., Jones C.W.; "Molecular analysis of the lac operon encoding the dependent lactose transport system and beta-galactc Agrobacterium radiobacter."; Mol. Microbiol. 6:1755-1768(1992).
                                                                                                                                                                                                                                                                              AGRRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
                                                                  MEDLINE=92334152; PubMed=1630315;
                                                                                 STRAIN-AR50;
                                                                                                SEQUENCE
                                                                                                                                        Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
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                                                                                                                                                                   Agrobacterium
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1993 (Rel.
2001 (Rel.
transport
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NOT_ANNOTATED_CDS.
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25, Last seq
40, Last ann
t ATP-binding
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39.7%;
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ling protein
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ein lacK.
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                           beta-galactosidase
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Q9Z3R9;
1 30-MAY-2000 (Rel. 39, Created)
I 01-MAR-2002 (Rel. 41, Last sequence update)
I 01-MAR-2002 (Rel. 41, Last annotation update)
I 01-MAR-2002 (Rel. 41, Last annotation update)
E Alpha-glucoside transport ATP-binding protein ac
N AGLK OR R00699 OR SMC03065.
SR Rhizobium meliloti (Sinorhizobium meliloti).
CC Bacteria; Proteobacteria; alpha subdivision; Rh
OC Rhizobiaceae; Sinorhizobium.
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Best Local S
Matches 138
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SMART; SM00382; AAA; 1.

PROSITE; PS00211; ABC_TRANSPORTER; 1.

Sugar transport; Transport; ATP-binding; Inner membrane.

NP_BIND 36 43 ATP (BY SIMILARITY).
                      SEQUENCE FROM N.A. MEDLINE=99328961;
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InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
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FOR LACTOSE. PROBABLY RE
TRANSPORT SYSTEM.
- SUBCELLULAR LOCATION: In
- SIMILARITY: BELONGS TO T
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     Walker
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THE ABC TRANSPORTER FAMI
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Pred.
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                                                                                                                                                                 subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 143;
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Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S. A. 98:9877-9882(2001).
-i- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR ALPHA-GLUCOSIDES SUCH AS SUCROSE, MALTOSE AND TREHALOSE.
PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
-i- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase and a periplasmic-binding-protein-dependent transport system for alpha-glucosides.";
J. Bacteriol. 181:4176-4184(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF045609; AAD12046.1; -. EMBL; AL591784; CAC45271.1; -.
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SMART; SM00382; AAA; 1.
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InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
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362
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Pred. No. 1.3e-38;
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-> P (IN REF. 1).
66B76CF47FE95A39 CRC64;
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EMBL; x54292; CAA38188.1; -.
EMBL; AE008897; AAL23054.1; -.
PIR; S05329; S05329;
PIR; S20602; S20602.
StyGene; SC10215; malk.
InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
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MEDLINE-89384443; PubMed=2674653;

Dahl M.K., Francoz E., Saurin W., Boos W., Manson M.D., Hofnung "Comparison of sequences from the malB regions of Salmonella "Comparison of sequences from the malB regions of Salmonella typhimurium and Enterobacter aerogenes with Escherichia coli KIZ potential new regulatory site in the interoperonic region.";

potential new regulatory site in the interoperonic region.";

Gen. Genet. 218:199-207(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92110387; PubMed-1730061; Schneider E., Francoz E., Dassa E., "Completion of the nucleotide sequence of the 'maltose B' Salmonella typhimurium: the high conservation of the malM suggests a selected physiological role for its product."; Blochim. Blophys. Acta 1129:223-227(1992).
                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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Grewal N., Mulvaney E.,
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P40790;
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01-MAR-2002 (Rel. 41, Last seque)
01-MAR-2002 (Rel. 41, Last annot spermidine/putrescine transport POTA OR STM1226.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma
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STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
Waterston R., Wilson R.K.;
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SMART; PS00211; ABC_TRANSPORTER; 1.
Transport; Sugar transport; Inner membrane;
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                                                 SEQUENCE OF 1-63 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=602;
                        MEDLINE-91258340;
                                                                                                                                         "Complete genome sequence
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    C.G.,
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141
  Miller J.L., Bagga [
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No. 3.6e-38;
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Best Local S
Matches 138
Escherichia.
NCBI_TaxID=562,
[1]
                                                                                                  MALK_ECOLI STANDARD; PRT; 371 AA.
P02914; Q47348;
21-JUL-1986 (Rel. 01, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Maltose/maltodextrin transport ATP-binding protein
MALK OR B4035 OR Z5633 OR ECS5018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and nucleotide sequence of the anaerobically regulated gene of Salmonella typhimurium.";
J. Bacteriol. 173:3554-3558(1991).
-I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SY FOR SPERMIDIME/PUTRESCIME. PROBABLY RESPONSIBLE FOR ENERGY
                                                                  Escherichia coli, and Escherichia coli 0157:H7.
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                                                   Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELULAR LOCATION: Inner membrane-associated, SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMIL CAUTION: Ref. 2 sequence differs from that shown frameshift in position 55.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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SEQUENCE FROM N.A.

STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21136231; PubMed-11258796;

MEDLINE-21136231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
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"Sequence of the malk gene in E.coli K12.";
Nucleic Acids Res. 10:7449-7458(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                      EXPRESSION.
SUBCELLULAR LOCATION: Inner membrane-associated.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Exteuropean Bioinformatics Institute. There are no rest European Bioinformatics Institutions as long as its content by non-profit institutions as long as its content fied and this statement is not removed. Usage by and
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STRAIN-RD / KW20 / ATCL JIV., MEDLINE-95350630; PubMed-7542800; MEDLINE-95350630; PubMed-7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
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Pred. No. 4.3e-38;
7; Mismatches 117;
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L -> P (IN REF. 1).
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InterPro; IPR003499; ABC_transpox
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER
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POTG_ECOLI
P31134;
                                                                                                                        01-JUL-1993 (Rel. 26, Created)
16-0CT-2001 (Rel. 40, Last sequen
16-0CT-2001 (Rel. 40, Last annota
Putrescine transport ATP-binding
POTG OR B0855.
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SEQUENCE
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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-I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT FOR IRON. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32698; AAC21800.1; TIGR; HI0126; -.
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"Whole-genome
NCBI_TaxID=562;
                                                                         Bacteria; Proteobacteria;
                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00211; ABC_TRANSPORTER; 1.
Iron transport; Transport; ATP-binding; Complete
NP_BIND 39 46 ATP (POTENTIAL).
SEQUENCE 328 AA; 36046 MW; 59B5298825D3597E C
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ABC_transportr.
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[2]
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InterPro; IPR003593; ABA.
InterPro; IPR003593; ABC_transportr.
InterPro; IPR003687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; I.
SMART; SM00382; ABA; I.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
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EMBL; AE000187; AAC73942.1; ALT_INIT.
EMBL; D90723; BAA35566.1; ALT_INIT.
PIR; B45313; B45313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto F. Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                       Transport; ATP-binding; Inner membrane; Complete proteome NP_BIND 52 59 ATP (BY SIMILARITY). SEQUENCE 377 AA; 41930 MW; 4C13E389C03CF76C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=93106992; PubMed=8416922;

Pistocchi R., Kashiwagi K., Miyamoto S., Nukui E., Sadakata Y.,

Pistocchi R., Igarashi K.;

Kobayashi H., Igarashi K.;

"Characteristics of the operon for a putrescine transport system

"Characteristics of the Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                       HSSP; P13569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061202; PubMed=8905232;
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80
                             64
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SUBCELLULAR LOCATION: Inner membrane-associated (PSIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
GVDLSQVPPYLRPINMMFQSYALFPHMTVEQNIAFGLKQDKLPKAEIASRVNEMLGLVHM
                                                                    SWISS-PROT entry is copyright. It is produced through
en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                          DTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQI 123
                                                       LEIRNLTKSYDGQHAVDDVSLTIYKGEIFALLGASGCGKSTLLRMLAGFEQPSAGQIMLD
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268:146-152(1993).
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Pred. No. 5
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O min region on the linkage
                                                                                                                  Mismatches
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Query Match Best Local S Matches 138

al Similarity 138; Conserv

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Score 611.5; DB 1 Pred. No. 6.5e-37; 6; Mismatches 130

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MEDLINE-97124196; PubMed-8969509;

YOShida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N
Miwa Y., Fujita Y.;

"Sequencing of a 65 kb region of the Bacillus subtilis genome
containing the lic and cel loci, and creation of a 177 kb contig
covering the gnt-sacxY region.";

Microbiology 142:3113-3123(1996).

-i- FUNCTION: INVOLVED IN A BINDING PROTEIN-DEPENDENT TRANSPORT

-i- FUNCTION: INVOLVED IN A BINDING PROTEIN-DEPENDENT TRANSPORT
                                        InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSMX_BACSU
P94360;
                                                                                                                                    SubtiList; BG11954; msmX.
                                                                                                                                                  EMBL; D83026;
EMBL; Z99123;
                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            modified and this statement is not removed
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                            Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Staphylococcus
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01-MAR-2002
                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                              RESPONSIBLE FOR THE UPTAKE OF MULTIPLE SUGARS (POTENTI SUBCELLULAR LOCATION: Membrane-associated (Potential). SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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1998 (Rel.
2002 (Rel.
multiple
                                                                                                                    IPR003593; AAA.
            Sugar transport; Membrane; ATP-binding; Complete 37 44 ATP (POTENTIAL).
 365 AA;
                                                                                                                                                  BAA11723.1; -. CAB15907.1; -.
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36, Last sequence update)
41, Last annotation update)
sugar-binding transport ATP-binding protein msmX.
41366 MW;
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          MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Kashimoto K., Kinura S., Kitakawa M., Kitagawa M., Kashamoto K., Kinura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCJV_ECOLI STANDARD; PRT; 322 AA. P77481; P76842; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical ABC transporter ATP-binding protein YCJV OR B1318.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIL** MG1555;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A.,

Blattner J.D., Railey M., Collado-Vides J., Glasner J.D., Re
Gregor J., Davis N.W., Kirkpatrick H.A., Ge
Gregor J., Davis N.W., Kirkpatrick H.A., Ge
Man B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98389658; PubMed=9721282; Fajardo D.A., Cheung J., Ito C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECOLI
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SIMILARITY:
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01-NOV-1997
01-NOV-1997
16-OCT-2001
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ECOGENE; EG13919; ycjv.

InterPro; IPR003439; ABA_transportr.

InterPro; IPR001687; ATP_GTP_A.

Pfam; PF00005; ABC_tran; 1.

SMART; SM00382; AAA; 1.

PROSITE; PS00211; ABC_TRANSPORTER; 1.
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 SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tai
Miyajima N., Hirosawa M., Sugiura
                                                                     Synechocystis sp. (strain Bacteria; Cyanobacteria; Cynobacteria; CynoBI_TaxID=1148;
                                                                                                                  Sulfate transport CYSA OR SLR1455.
                                                                                                                                                                                                                      SYNY3
                                                                                                                                                                                                        CYSA_SYNY3
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1 (Rel. 40, Last anno
ansport ATP-binding p
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35766 MW;
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   Sugiura M.,
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67; Mismatches
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               Tanaka
                                                                                                                                                                                                                                                                              306
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cysA.
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 A., Asami
Sasamoto
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hes 99;
                                                                                      Synechocystis
 Asamizu 1
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Best Local 9
SMOK_RHOSH STANDARD;
p54933; 0310834;
01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last seque
16-OCT-2001 (Rel. 40, Last annot
ATP-binding transport protein sn
SMOK OR POLK.
Rhodobacter sphaeroides (Rhodops
                                                                                                                                                                                                                                    RHOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. NP_BIND 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00005; ABC_tran; 1. SMART; SM00382; AAA; 1.
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InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
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Yamada M., Yasuda M.,
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mes 133; Conser
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FUNCTION: INVOLVED IN THE TRANSPORT OF MULTIPLE SULFUR-CONTAINING COMPOUNDS, INCLUDING SULFATE AND THIOSULFATE (BY SIMILARITY).

SUBCELLULAR LOCATION: Inner membrane-associated (Potential).

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GITTYYYTHDQEEAMAISDQIAVMKDGYIQQIGRPKELYHKPANEFYATFIGRTNIIPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEFYFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQDATHVDIRKRNIGFVFQHYALFKHLTIRQNIAFGLEIRKHPPAKTKERVEELLSLIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIINNVSKQFGDETALKDINLEVPDGKLVALLGPSGSGKSTLLRAIAGLEEPDQGQIIIN
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                                                                                                                                                                                                                                                                                                                                                            LG-----
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Shimpo S., Takeuchi C., Wada T., Watanabe A.,
ssuda M., Tabata S.;
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39195 MW;
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                                                                                    Last sequence update)
Last annotation updat
   (Rhodopseudomonas sphaeroides).
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Pred. No. 4.2e-36;
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; 34CB746CD68E7EB7
                                                               SmoK
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                                                                                                                                                                                                            PRT;
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                                                            cion update) ( (PolK).
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RESULT 15
Y4OS_RHISN
ID Y4OS_R
ID 174OS_R
AC P55604
DT 01-NOV
DT 16-OCT
DE Probab
GN Y4OS.
OS Rhizob
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      Rhizobium
                                                               Probable
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Query Match
Best Local Similarity
                                                            01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                            Y40S_RHISN
P55604;
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J. Bacteriol. 179:6335-6340(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Transport.
NP_BIND 36 43
SEQUENCE 332 AA; 3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stein M.A., Schafer A., Giffhorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
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                                                                                                                                                                                                                                                                                           TIRDSVYLGLNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADG
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                                                                                                                                                                                                                                                    EVGVSEHLG---SDTFLHVHVAGMPTLTVRTGGEFGVHHGDRVWLTPQADKIHRFGADG
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                                             ABC
sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 AA; 36362 MW;
                                                            (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                        (Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
transporter ATP-binding protein
    (strain
                                                                                                                                                 STANDARD;
                                                            35,
35,
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                                                                                                      Created)
      NGR234).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                      SPKMNLIEGPEAAKHGATTIGIRPEHIDLSREAGAWEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 599; DB 1;
Pred. No. 4.5e-36;
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                                                                                                                                                 PRT;
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                                                                                                                                                 371
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Search completed: July 30, Job time: 222 sec
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Best Local Similarity
Matches 135; Conserv
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InterPro; IPR003439; ABC_transportr.

InterPro; IPR001439; ABC_transportr.

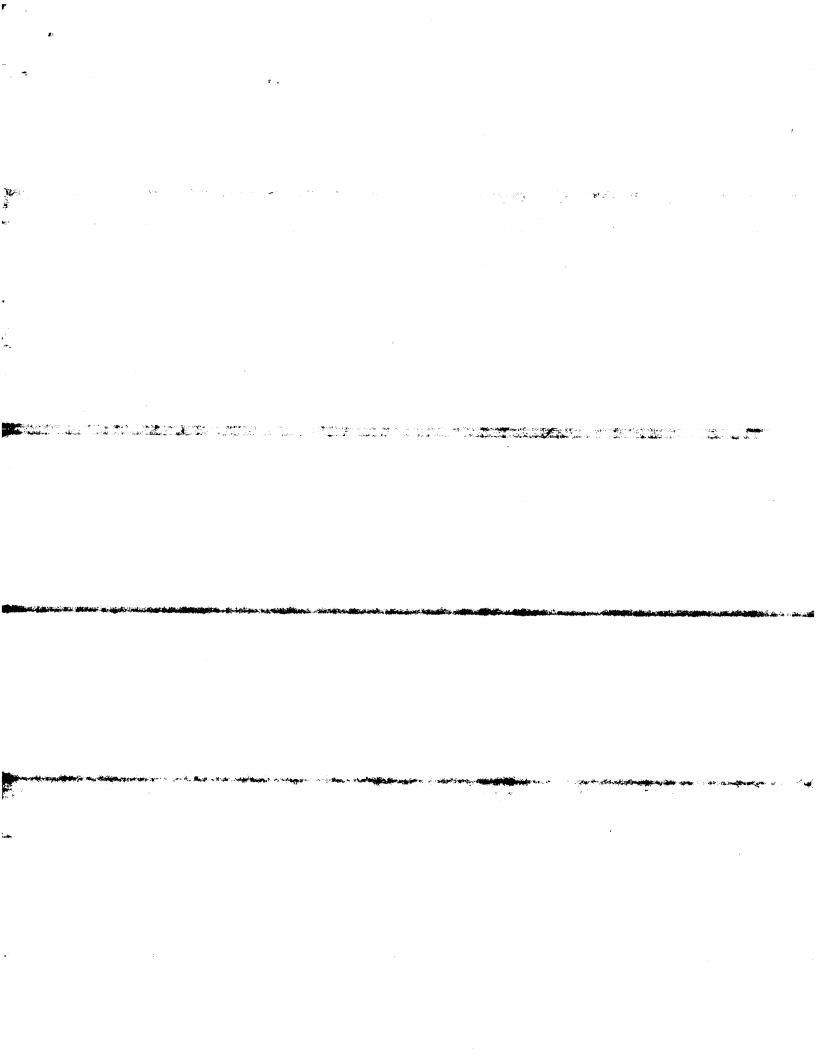
InterPro; IPR001687; AIP_GTP_A.

Pfam; PF00005; ABC_tran; 1.

PF00005; ABC_tran; 1.

PROSITE; PS00211; ABC_TRANSPORTER; 1.

PROSITE: PS00211; ABC_TRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular basis of symbiosis between Rhizobium and legumes.";
nature 387:394-401(1997).
-i-FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM Y40PQRS. THIS SYSTEM PROBABLY TRANSPORTS A SUGAR-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000089; AAB91805.1; -.
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Q988zO rhizobium l		Q9rut0 deinococcus	Q9v306 thermococcu	P96483 streptomyce	Q9hh32 pyrococcus						vibrio cho	P73468 synechocyst	a		Q9i6t2 pseudomonas			Q92100 rhizobium m	pyrococcus	Q9yq58 aeropyrum p	Q9kdy5 bacillus ha		pyrococcu	051587 borrelia bu	Q9v2q1 pyrococcus	Q92xf6 rhizobium m	2ng2 rhizobium	Q9ckz6 pasteurella

ALIGNMENTS

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DY OLYST2 PRELIMINARY; PRT; 363 AA.
AC G97ST2;
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DCC-2001 (TrEMBLrel. 19, Last sequence update)
DE ABC TRANSPORTER, ATP-BINDING PROTEIN.
SP0242.
OS Streptococcus pneumoniae.
OC Streptococcus.
OC Streptococcus.
OC Streptococcus.
OC Streptococcus.
OX NOBL TAXID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE-21357209; pubMed-11463916;
RX MEDLINE-21357209; pubMed-
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Local Similarity

BB 16;

Length

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Best Local S
Matches 363
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-20025807; PubMed-10559160;

MEDLINE-20025807; PubMed-10559160;

Dugourd D., Martin C., Rioux C.R., Jacques M., Harel J.;

"Characterization of a periplasmic ATP-binding cassette
"Characterization of a periplasmic ATP-binding cassette
system of Brachyspira (Serpulina) hyodysenteriae.";

J. Bacteriol. 181:6948-6957(1999).
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054370;
                                                                                                                                                                                          ATP-binding; Transpance 374 AA;
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INTERPRO; IPR003593; AAA.

INTERPRO; IPR003439; ABC_transportr.

INTERPRO; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema hyodysenteriae (
Bacteria; Spirochaetales;
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01-JUN-1998 (TrEMBLrel. 06, La
01-DEC-2001 (TrEMBLrel. 19, La
PUTATIVE ABC TRANSPORTER BITD.
                                                                                                                                                                                                                                               PROSITE;
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SMART; SM00382; AAA; 1.
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ISIENVVKRYEKLTIIPDLSLEIKNGEFFTLLGPSGCGKTTLLRWIAGFNTIEGGEIKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGLNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNLIKGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGLNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNLIKGVN
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                                                                                                             Similarity
                                                                                                                                                                                                                                          PS00211; ABC_TRANSPORTER;
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                                                                                      Conservative
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                                                                                                           49.9%;
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Brachyspiraceae; Brachysp
                                                                                        65;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                      Score 919; DB 2;
Pred. No. 1.3e-53;
5; Mismatches 103
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Pred. No. 3.1
0; Mismatches
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QΥ В Qy

61

Y FDDTK I NNMEPSKRNIGMV FQNYAI FPHLTVRDNVAFGLMQKKVPKEEL I QQTNKYLEL MAQVKIDGVKKYFGNVRALDGIDLVVNEGEFLVLLGPSGCGKTTLLRCIAGLEQVTGGKI MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF

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 Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                         MEDIINE-99287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Tyvidence for lateral gene transfer between Archaea and Bacteria fro
                                                                      InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Complete proteome; Transport.
SEQUENCE 355 AA; 39814 MW; 44F330C0316CE3EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9X0V9;
                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO 7 (ABC TRANSPORTERS).
EMBL; AE001779; AAD36307.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
SUGAR ABC TRANSPORTER, ATP-BINDING PROTEIN.
                                                                                                                                                                                                                                                  genome sequence of Thermotoga maritima.";
Nature 399.323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima.
Bacteria; Thermotogales;
                                                                                                                                                                                           TIGR; TM1232;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                           InterPro; IPR003593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQI 123
||||: ||||||||||||:|||:|| :|| :| :: :: | :::|
KDVINNIPAHKRNIGMVFQNYAIFPHMTVRENVEYGLKLRKENKESMKKKVDEMLHVVKI 124
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                                                                                                                                                                                                                                                                                                                                                                                                  3109;
             38.8%;
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Score 714.5;
Pred. No. 5.26
32; Mismatches
                                                                                                                                                                                                                                      ATP-BINDING
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0.2e-40;
les 125;
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                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 138
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MEDLINE-99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria

genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; TM1376; ...
InterPro; IPR003593; AAA.
InterPro; IPR003499; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotoga maritima.
Bacteria; Thermotogales;
NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Complete proteome; SEQUENCE 368 AA; 42046 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                            123
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FFNDRDVTNLPPKDRNISMVFQSYAVWPHMKVYDNIAYPLKLKKVPKEEIEKRVKWAADL
                                                                                                        DDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLELMQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVYFAEKLMSDTILHLNVGSE-KIVAKIPGDVDFRSGEKITFFLDVEKIHLFHPETGERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVYLG--LNTDYFIETGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADGSQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLEMEVRSEGNSVVLQNG-EIKIPAKTDPGAKKVILGIRPENVYLEEKPNTLKLEG----
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                                                                                                                                                                            EVSIKNVSKFFDDFQVLKNVSLDIKKGEFFSILGPSGCGKTTLLRVIAGFEGVESGDVLL
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                                                                           DGKSILNLPPNKRPVNIIFQNYALFPHLTVFENIAFPLKLKKLSENEINQRVNELLSLIR
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                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                       38.0%;
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                                                                                                                                                                                                                                                                          75;
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Last annotation update)
RANSPORTER, ATP-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                     : Transport.
89954C183F611C9C
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                       701; DB 16;
No. 4.3e-39;
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                                                                                                                                                                                                                                                                                                                            Length 368;
                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrett M.M.,
Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White O.,
                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                          Gaps
                          182
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Best Local :
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SUGAR-BINDING TRANSPORT ATP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-20566786; PubMed-11115105;
MIDITURGE J., Dunn D., Maeder D.L., Holley-Shan
Horlacher R., Robb F.T., Boos W., Weiss R.B.;
"Evidence of recent lateral gene transfer among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00005; ABC_t:
SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MO1. Microbiol. 38:684-693(2000).
EMBL; AF307052; AAG45383.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota;
NCBI_TaxID=2261;
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IPR003439; ABC_transportr.
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Pred. No. 2.
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O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

FUTATIVE ATP-BINDING ABC TRANSPORTER PROTEIN.

SMC01608.

Rhizobium meliloti (Sinorhizobium meliloti).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiac Rhizobiaceae; Sinorhizobium.
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MEDLINE=20566786; PubMed=11115105;
Diruggiero J., Dunn D., Maeder D.L., Holley-Shanks R.,
Horlacher R., Robb F.T., Boos W., Weiss R.B.;
"Evidence of recent lateral gene transfer among hyperth
archaea.";
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Q9HH23;
Q1-MAR-2001 (TrEMBLrel. 16, Creat
Q1-MAR-2001 (TrEMBLrel. 17, Last
Q1-JUN-2001 (TrEMBLrel. 17, Last
PUTATIVE SUGAR-BINDING TRANSPORT
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
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Archaea; Euryarchaeota;
NCBI_TaxID=2265;
    SEQUENCE FROM
                                             NCBI_TaxID=382;
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EMBL; AF307053; AAG45398.1; -.
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A Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
A Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
A Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
A Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
A Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
A Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
A Masuy D., Palm C., Peck W.C., Pohl T.M., Portetelle D., Purnelle B.,
A Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
A Norhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
A Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
A Science 293:668-672(2001).
B EMBL, AL591790; CAC46799.1; -.
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01-DEC-2001 (TremBLrel. 1:
358AA LONG HYPOTHETICAL TH
APE1732.
MEDLINE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., K Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix KI.";
                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=K1;
                                                                                                                                                                                              NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                         Q9YB65;
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142; Conser
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43.8%;
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12, Last sequence update)
19, Last annotation updat
TRANSPORTER ATP-BINDING P
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Pred. No. 3.5e
65; Mismatches
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Best Local Similarity
Matches 145; Conserv
STRAIN-569B;
STRAIN-569B;
Butta P.P., Roychoudhury S., Chaudhuri K.;
"Probable Malk protein of Vibrio cholerae.'
Submitted (APR-2000) to the EMBL/GenBank/Di
EMBL; AF259974; AAF70304.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
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Q9L531;
01-OCT-2000
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PROSITE; PS00211; ABC_TRANSPORTER;
PROSITE; PS00059; ADH_ZINC; 1.
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InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
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HSSP; Q58663; 1G6H.
InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
                                                                                                                                                                                                      Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                MALK
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=666;
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ATP-BINDING TRANSPORT PROTEIN FAMILY
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           SMART; SM00382; AAĀ; 1.

PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.

ATP-binding; Complete proteome.

SEQUENCE 373 AA; 41404 MW; A15E521894CABA
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InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.

A15E521894CABA55

TIGR; VCA0946;

InterPro;

IPR003593; AAA.

Nature 406:477-483(2000). EMBL; AE004421; AAF96842.1;

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RESULT
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Best Local
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        [1]
SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE O1;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,
Ermolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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SMART;
"DNA sequence of both chromosomes of the cholerae.";
                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MALTOSE/MALTODEXTRIN ABC TRANSPORTER, ATP-BINDING P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1. ATP-binding.
SEQUENCE 373 AA; 41404 MW; BDAC521894CABA
                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
                                                                                                                                                                                                                                                                       NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVMIVEKLGNETQVYMNLKGSDSDVIYRQPDTL--DVETGDTLTIGIPAHRCHLFHSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEVGITTVYVTHDQEEAMAISDQIAVMKDGVIQQIGRPKELYHKPANEFVATFIG--RTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIRDSVYLGLNTDYFIE-TGFASKIQVSEESTFEEDLQKGNRIRLRINTQKLNIFSADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMSVFIEGVEKDRVQVQLSNGTTFWIPVDGTTVTRGERMSLGIRPEHLVEAEHGDAKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIPANLE-KRSDGAYIVFSDGYALRMP--ALDQVEEQAIHVSIRPEEFIKDESGD--IEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKLGCTMIYVTHDQVEAWTMADKIVVLDAGFVSQVGKPLELYHYPQNRFVAGFIGSPKMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIGEQRMNDVEPSKRGVGMVFQSYALYPHLNLYDNMSFGLKLSKADKSEIKKRVDHAAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFDDTKINNMEPSKRNIGMVFQNYAIFPHLTVRDNVAFGLMQKKVPKEELIQQTNKYLEL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASVTLKNVCKAYGDVLISKNVDLEIQEGEFVVFVGPSGCGKSTLLRCIAGLEDITSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00005; ; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138;
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                                                                                                                                                                                                                                                                                           Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC_tran;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36
38
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                                                                                                                                                                                                                                                                                           gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 668; DB Pred. No. 7e-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BDAC521894CABA55
                                                                                                                                                                                                                                                                                             subdivision;
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Query Match Best Local Similarity

36.2%;

Length 373;

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RESULT
Q9HKB3
ID Q9HKB3
ID Q9
AC Q9
AC Q9
DT 01

B
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Best Local
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                                                                                                                                                                                                                  InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003439; ABC_tran;
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMARF; SM00382; AAA; 1.
SMARF; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Complete proteome; TransposedueNce 372 AA; 41642 MW; 2F37EC38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20479972; PubMed-11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HKB3 PRELIMINARY; PRT; 372 AA.
Q9HKB3;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE SUGAR ABC TRANSPORTER, ATP-BINDING PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TA0688.
Thermoplasma acidophilum.
Thermoplasmales;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 407:508-513(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-DSM 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABC
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                                              MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
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MSVI-IENLTARYGDKYILKNENLRVEDGEFFVILGSSGSGKTTLLRSIAGLIPIDDGRI 59
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                                                                                                  al Similarity
149; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                           ABC TRANSPORTERS).
AL445065; CAC11826.1;
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                                                                                                  Conservative
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Pred. No. 7e-37;
                                                                                             Score 662.5;
Pred. No. 1.6e
72; Mismatches
                                                                                                                                                                                                                        ; Transport.
2F37EC38218AE4B9 CRC64;
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                                                                                                .6e-36;
les 125;
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                                                                                                                                               DB 17;
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; pF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS000211; AAA; 1.
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ATP-binding; Transport.
SEQUENCE 397 AA; 42352 MW; 11D6EES
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St. ACEI_TaxID=1902;
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-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMEMBL; AL031225; CAA20221.1; -.
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MEDLINE=97000351; PubMed=8843436;
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Parkhill J.,
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01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
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Query Match
Best Local Similarity
Matches 142; Conserv

Conservative

76;

Score 661.5; DB 2 Pred. No. 2.1e-36; 6; Mismatches 134

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Gaps

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35.9**%**; 38.3**%**;

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01-AUG-1998 (TREMBLREL (
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohf
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InterPro; IPR001687; ATP_GTP_A.
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Archaea; Euryarchaeota;
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                                            MSEIKIINAKKIYHDVPVIENLNITIPKGSLFTLLGASGCGKTTLLRMIAGFNSIEGGEF
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07, Last sequence update)
17, Last annotation update)
MULTIPLE SUGAR-BINDING TRAN
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ismatches 108;
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hfuku Y.,
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L K.,
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Q49978;
01-NOV-1996
                                            InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                              Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S. Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M. Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares F., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1. ATP-binding; Complete proteome. SEQUENCE 392 AA; 42775 MW; 7123DF2D7C87BF
                                                                                                                     "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
EMBL; U15180; AAA62878.1; .
EMBL; AL583920; CAC31470.1; -.
Leproma; ML1089; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria;
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01-DEC-2001
                                                                                                                                                                                                     Squares S., S
Barrell B.G.;
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yv-1996 (TrEMBLrel. 01, Last sequence update)
EC-2001 (TrEMBLrel. 19, Last annotation update)
(PROBABLE ABC-TRANSPORT PROTEIN, ATP-BINDING C
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   7123DF2D7C87BFDF
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Mycobacteriaceae; M
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    CRC64;
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Query Match Best Local Similarity

35.7%; 38.7%;

Score Pred.

658.5; DB 1

DB 16;

Length

Mat:ches

153;

Conservative

57;

Mismatches

134;

Indels

51;

Gaps

10;

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STRAIN-MSB8 / DSM 3109;

RX MEDLINE-99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA McDonald L., Octton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;

RT Styldence for lateral gene transfer between Archaea and Bacteria from

RT Grome sequence of Thermotoga maritima.";

RL Nature 399:323-329(1999).

DR EMBL; AE001783; AAD36351.1; -.

PR TIGR; TM1276; -.
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                                                                             Query Match
Best Local 9
                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9X103 PRELIMINARY;
O9X103;
O1-NOV-1999 (TrEMBLrel. 12, C.
O1-NOV-1999 (TrEMBLrel. 12, L.
O1-UN-2001 (TrEMBLrel. 17, L.
SUGAR ABC TRANSPORTER, ATP-BI
TM1276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima.
Bacteria; Thermotogales;
CBI_TaxID=2336;
                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.ATP-binding; Complete proteome.
SEQUENCE 369 AA; 41539 MW; AA589E22C2A56F
                                                                                                                                                                                                                                                               Pfam; PF00005; ABC_tran; 1. SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr
InterPro; IPR001687; ATP_GTP_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARVSAESKMAIGESIELAFGTAKIAVFDADSGVNL
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147; Conservative
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                                                                             35.7%;
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                                                    72;
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Last annotation update)
                                              Score 657.5; I
Pred. No. 3.4e<sup>-</sup>
72; Mismatches
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                                                                                                                                                                                     AA589E22C2A56F43 CRC64;
                                                                       No. 3.
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VLDMTRMHAFDKETEKAII
            RINTQKLNIFSADGSQNLI::::::|
                                                           ---SGDIEGTIRDSVYLGLNTDYFIETG----FAS----KIQVSEESTFEEDLQKGNRIRL
                                                                                         NFVNARV-VRGEGGLWIQASGFKVKVPKEFEDKLANYIDKEIIFGIRPED-IYDKLFALA
                                                                                                               NIIPANLEKRSDGAYIVFSDGYALRMP-----ALDQVEEQAIHVSIRPEEFIKDE----
                                                                                                                                                                                  ILGIENLLDRKPRQLSGGQRQRVAVGRAIVRNPKVFLFDEPLSNLDAKLRVQMRSELKKL
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369
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Search completed: July 30, 2002, 15:51:35 Job time: 228 sec

